

FIGURE 72

CAGCCCCGCGCGCCGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCGCGCCCTTCACGCTG
CCCCCTCCGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGAGCCCGGAGCCCC
TGCCGAGCGCACGCGACGGCTTGGCGCTCGCCCTGGAGCTGCGCTGGCGTCCCCGCGG
GCGCCGCCAACTTCTTGGCATTGTTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGTTATACCCCTATTAAAGGAAGAGTGGTACTACCAGATAGAAATTTCTG
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCTGGACAGTGGCACCACGCTGCTGCGCCTGCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTGGAACACCTTGGTCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCTGCCTCAGCTTTACATTACG
CCATGATGGGGGCCGGCTGAATTATGAATGTTACCGATTCCGGCATTTCCCCATCCACAAAT
GCGCTGGTGTATCGGTGCCACGGTGTATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGACAGCGAGCCCCGTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCGTGACCCTGAGGTCGTCA
ATGATGAGTCCTCTCTGGT CAGACATCGCTGGAATTGAATAGCCAGGCGTGACCTCAAGCAA
CCATGAATCAGCTATTAAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGCTTCAATCTCTGTTCTGCTCCGATGCGCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAAACCTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTAERHADGLAL
ALEPALASPAGAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESNF
FLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTLLLR
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISIIYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
ETAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLLPFRCL
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCGCAGCGCCGTGG
TCAGGGGCGCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGAGCG
CGCGTGGTGTGCGCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCTATCTTCATGGCCTTGGAAGTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCGCTTGCTGAAGGCATGTGCCCTTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCCACTGTGCGGGGAGCTCTTGACTTCAAACGCTTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGAGCTCGCCAAACAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCACC
CAGGCGCTGTGAACCTCGAGCTGTTCTGCGCCATGTTCTGAGTGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGTCTCGGGCACCAGAGGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAG
AGGTGCCTCCAGCTGCGCGAGACGACCGGCGAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGAGGATGCTGAACCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCATCTTCTCTAAGCACCCCCACCCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCTTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCCT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCAAGCTGTGCCCTGGACATCTCTTTCTGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCCTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGCTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCTTCGGGGCGG
ATGCAGGGCTGGGGTCTCTGTATCTGAAGCCCTCGGAATAAGCGCGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAAA

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